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Sequence Listing could not be accepted.

If you need help call the Patent Electronic Business Center at (866) 217-9197 (toll free).

Reviewer: Anne Corrigan

Timestamp: [year=2010; month=1; day=19; hr=10; min=55; sec=46; ms=248;]

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Reviewer Comments:

<210> 1

<211> 776

<212> PRT

<213> mammalian

The above <213> response is invalid, per 1.823 of the Sequence Rules. The only valid responses are: the Genus species of the organism, "Artificial Sequence," or "Unknown". "Artificial Sequence" and "Unknown" require explanation in the <220>-<223> section; please indicste the source of the genetic material. For example, "mammalian" would be an acceptable explanation for "Unknown". Same error in Sequence 2.

<210> 11

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<223> peptide

<400> 11

As an explanation of "<213> Artificial Sequence", the above <223> response is insufficient. The sequence is obviously a peptide sequence. Please indicate the source of the genetic material; same error in Sequences 12-14.

Application No: 10568396 Version No: 3.0

Input Set:

Output Set:

Started: 2009-12-30 18:59:37.288
Finished: 2009-12-30 18:59:38.532
Elapsed: 0 hr(s) 0 min(s) 1 sec(s) 244 ms
Total Warnings: 14
Total Errors: 0
No. of SeqIDs Defined: 14
Actual SeqID Count: 14

| Error code | Error Description |
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| W 402 | Undefined organism found in <213> in SEQ ID (1) |
| W 402 | Undefined organism found in <213> in SEQ ID (2) |
| W 213 | Artificial or Unknown found in <213> in SEQ ID (3) |
| W 213 | Artificial or Unknown found in <213> in SEQ ID (4) |
| W 213 | Artificial or Unknown found in <213> in SEQ ID (5) |
| W 213 | Artificial or Unknown found in <213> in SEQ ID (6) |
| W 213 | Artificial or Unknown found in <213> in SEQ ID (7) |
| W 213 | Artificial or Unknown found in <213> in SEQ ID (8) |
| W 213 | Artificial or Unknown found in <213> in SEQ ID (9) |
| W 213 | Artificial or Unknown found in <213> in SEQ ID (10) |
| W 213 | Artificial or Unknown found in <213> in SEQ ID (11) |
| W 213 | Artificial or Unknown found in <213> in SEQ ID (12) |
| W 213 | Artificial or Unknown found in <213> in SEQ ID (13) |
| W 213 | Artificial or Unknown found in <213> in SEQ ID (14) |

SEQUENCE LISTING

<110> THE TRUSTEES OF COLUMBIA UNIVERSITY IN THE CITY OF NEW YORK

<120> ZAP PROTEIN AND RELATED COMPOSITIONS AND METHODS

<130> 67489-PCT/JPW/JW

<140> 10568396

<141> 2006-08-31

<150> PCT/US2004/026162

<151> 2004-08-12

<160> 14

<170> PatentIn version 3.5

<210> 1

<211> 776

<212> PRT

<213> mammalian

<400> 1

Met Ala Asp Pro Gly Val Cys Cys Phe Ile Thr Lys Ile Leu Cys Ala
1 5 10 15

His Gly Gly Arg Met Thr Leu Glu Glu Leu Leu Gly Glu Ile Arg Leu
20 25 30

Pro Glu Ala Gln Leu Tyr Glu Leu Leu Glu Thr Ala Gly Pro Asp Arg
35 40 45

Phe Val Leu Leu Glu Thr Gly Gly Gln Ala Gly Ile Thr Arg Ser Val
50 55 60

Val Ala Thr Thr Arg Ala Arg Val Cys Arg Arg Lys Tyr Cys Gln Arg
65 70 75 80

Pro Cys Asp Ser Leu His Leu Cys Lys Leu Asn Leu Leu Gly Arg Cys
85 90 95

His Tyr Ala Gln Ser Gln Arg Asn Leu Cys Lys Tyr Ser His Asp Val
100 105 110

Leu Ser Glu Gln Asn Phe Gln Ile Leu Lys Asn His Glu Leu Ser Gly
115 120 125

Leu Asn Gln Glu Glu Leu Ala Cys Leu Leu Val Gln Ser Asp Pro Phe
130 135 140

Phe Leu Pro Glu Ile Cys Lys Ser Tyr Lys Gly Glu Gly Arg Lys Gln
145 150 155 160

Thr Cys Gly Gln Pro Gln Pro Cys Glu Arg Leu His Ile Cys Glu His
165 170 175

Phe Thr Arg Gly Asn Cys Ser Tyr Leu Asn Cys Leu Arg Ser His Asn
180 185 190

Leu Met Asp Arg Lys Val Leu Thr Ile Met Arg Glu His Gly Leu Ser
195 200 205

Pro Asp Val Val Gln Asn Ile Gln Asp Ile Cys Asn Asn Lys His Ala
210 215 220

Arg Arg Asn Pro Pro Gly Thr Arg Ala Ala His Pro His Arg Arg Gly
225 230 235 240

Gly Ala His Arg Asp Arg Ser Lys Ser Arg Asp Arg Phe Leu His Asn
245 250 255

Ser Leu Glu Phe Leu Ser Pro Val Val Ser Pro Leu Gly Ser Gly Pro
260 265 270

Pro Ser Pro Asp Val Thr Ser Cys Lys Asp Ser Leu Glu Asp Val Ser
275 280 285

Val Asp Val Thr Gln Lys Phe Lys Tyr Leu Gly Thr His Asp Arg Ala
290 295 300

Gln Leu Ser Pro Val Ser Ser Lys Ala Ala Gly Val Gln Gly Pro Ser
305 310 315 320

Gln Met Arg Ala Ser Gln Glu Phe Ser Glu Asp Gly Asn Leu Asp Asp
325 330 335

Ile Phe Ser Arg Asn Arg Ser Asp Ser Ser Ser Ser Arg Ala Ser Ala
340 345 350

Ala Lys Val Ala Gln Arg Asn Glu Ala Val Ala Met Lys Met Gly Met

355

360

365

Glu Val Lys Gly Lys Lys Glu Ala Pro Asp Ile Asp Arg Val Pro Phe
370 375 380

Leu Asn Ser Tyr Ile Asp Gly Val Thr Met Glu Lys Ala Ser Val Ser
385 390 395 400

Gly Ile Pro Gly Lys Lys Phe Thr Ala Asn Asp Leu Glu Asn Leu Leu
405 410 415

Leu Leu Asn Asp Thr Trp Lys Asn Val Ala Lys Pro Gln Asp Leu Gln
420 425 430

Thr Thr Gly Arg Ile Thr Asp Ser Gly Gln Asp Lys Ala Phe Leu Gln
435 440 445

Asn Lys Tyr Gly Gly Asn Pro Val Trp Ala Ser Ala Ser Thr His Asn
450 455 460

Ala Pro Asn Gly Ser Ser Gln Ile Met Asp Glu Thr Pro Asn Val Ser
465 470 475 480

Lys Ser Ser Thr Ser Gly Phe Ala Ile Lys Pro Ala Ile Ala Gly Gly
485 490 495

Lys Glu Ala Val Tyr Ser Gly Val Gln Ser Pro Arg Ser Gln Val Leu
500 505 510

Ala Val Pro Gly Glu Ala Thr Thr Pro Val Gln Ser Asn Arg Leu Pro
515 520 525

Gln Ser Pro Leu Ser Ser Ser Ser His Arg Ala Ala Ala Ser Gly Ser
530 535 540

Pro Gly Lys Asn Ser Thr His Thr Ser Val Ser Pro Ala Ile Glu Ser
545 550 555 560

Ser Arg Met Thr Ser Asp Pro Asp Glu Tyr Leu Leu Arg Tyr Ile Leu
565 570 575

Asn Pro Leu Phe Arg Met Asp Asn His Gly Pro Lys Glu Ile Cys Gln
580 585 590

Asp His Leu Tyr Lys Gly Cys Gln Gln Ser His Cys Asp Arg Ser His
595 600 605

Phe His Leu Pro Tyr Arg Trp Gln Met Phe Val Tyr Thr Thr Trp Arg
610 615 620

Asp Phe Gln Asp Met Glu Ser Ile Glu Gln Ala Tyr Cys Asp Pro His
625 630 635 640

Val Glu Leu Ile Leu Ile Glu Asn His Gln Ile Asn Phe Gln Lys Met
645 650 655

Thr Cys Asp Ser Tyr Pro Ile Arg Arg Leu Ser Thr Pro Ser Tyr Glu
660 665 670

Glu Lys Pro Leu Ser Ala Val Phe Ala Thr Lys Trp Ile Trp Tyr Trp
675 680 685

Lys Asn Glu Phe Asn Glu Tyr Ile Gln Tyr Gly Asn Glu Ser Pro Gly
690 695 700

His Thr Ser Ser Asp Ile Asn Ser Ala Tyr Leu Glu Ser Phe Phe Gln
705 710 715 720

Ser Cys Pro Arg Gly Val Leu Pro Phe Gln Ala Gly Ser Gln Lys Tyr
725 730 735

Glu Leu Ser Phe Gln Gly Met Ile Gln Thr Asn Ile Ala Ser Lys Thr
740 745 750

Gln Arg His Val Val Arg Arg Pro Val Phe Val Ser Ser Asn Asp Val
755 760 765

Glu Gln Lys Arg Arg Gly Pro Glu
770 775

<210> 2
<211> 2331
<212> DNA
<213> mammalian

<400> 2
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| | |
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| ctggagacgg cggggcccg tgcgttcgtg ctattggaga ctggaggcca ggccgggatc | 180 |
| actcggctctg tagtggctac tactcgagcc cgcgtctgcc gtcggaagta ctgccagaga | 240 |
| cctgcgaca gcctgcacct ctgcaagctt aatctgctcg gccggtgcc statgcacag | 300 |
| tctcagcggg acctctgcaa atattctcac gatgttctct cggaacagaa cttccagatc | 360 |
| ctgaagaatc atgagctctc tgggcttaac caagaggagc tagcttgcc cctggtccaa | 420 |
| agcgaccctt ttttctgcc cgagatatgc aagagttaca aaggagaggg ccgaaaacag | 480 |
| acctgtgggc agccacagcc atgcgagaga ctccacatct gtgagcaact caccggggc | 540 |
| aactgcagtt acctcaactg tctcaggtct cacaacctga tggacagaaa ggtgttgacc | 600 |
| atcatgaggg agcacgggct gagtctgat gtggtccaga acatccagga catctgcaac | 660 |
| aacaaacacg ccaggaggaa cccgcctggc acgagagctg cccatccaca ccgcagaggc | 720 |
| ggcgcacaca gagacagaag caaaagcaga gaccgcttcc ttcacaacag tctagaat | 780 |
| ctctcacctg ttgtctcacc tctgggatct ggtccgcta gccagatgt caccagctgt | 840 |
| aaagattccc tggaggatgt gtctgtggat gtcaccaga agttcaagta cttggggacg | 900 |
| catgaccgtg cgcagctctc ccagttctca tctaaggctg ctggtgttca aggaccagt | 960 |
| caaatgagag caagccaaga gttttcagag gatgggaatc tagatgacat attttctagg | 1020 |
| aatcgttctg attcatcatc aagtcgagcc tccgctgcc aggtggcaca aagaaatgaa | 1080 |
| gctgtggcca tgaaaatggg catggaggtc aagggcaaga aggaggctcc agacatcgat | 1140 |
| cgggtcccat ttttaaatag ttatattgat ggggtgacca tggaaaaagc atcgttctca | 1200 |
| ggaattccag gcaaaaagtt cacagccaat gatctggaaa atttgctatt acttaacgac | 1260 |
| acttgaaga atgtggctaa gcccaggat ctgcagacca caggcagaat cactgacagt | 1320 |
| ggccaagaca aggcattcct gcagaataaa tatggaggaa acccagtgtg ggcaagtgca | 1380 |
| tccaccata atgccccaaa tggtcttagt caaattatgg atgaaactcc taatgtctct | 1440 |
| aaaagtagta ccagtggttt tgccataaaa ccagcaattg ctggaggaaa agaagcagtc | 1500 |
| tattctggag ttcagagtcc gagaagccag gtcctagctg tgcttgggga ggctactacc | 1560 |
| cctgtacaga gcaacaggct gcctcagtcg cctctgtctt cctcaagcca cagagctgca | 1620 |
| gcctctggga gccctggcaa gaactccacc catacctctg tgagcccagc catcgagtct | 1680 |
| tcaaggatga catcagacc cgatgagtat ctctacgct acatcctaaa tcctttat | 1740 |

| | |
|--|------|
| aggatggata atcatggccc gaaggaaatc tgtcaggacc atctgtacaa gggctgtcaa | 1800 |
| cagagccact gcgacaggag tcacttccat ctgccctacc ggtggcagat gttcgtatat | 1860 |
| accacttggga gggacttcca ggacatggag tctatcgaac aggcctattg tgatccccac | 1920 |
| gttgaactca ttttgataga aaaccatcag atcaatttcc agaaaatgac ctgtgactcc | 1980 |
| taccccatcc gacgcctctc cactccctca tatgaggaaa agccacttag tgctgtcttc | 2040 |
| gccaccaagt ggatttggtg ttggaagaat gaatttaatg aatatatcca gtatgggaat | 2100 |
| gagagcccag gccacaccag ctctgacatc aactctgcgt acctggagtc tttcttccag | 2160 |
| tcttgtccca ggggagtttt gccattccag gctgggtcac agaagtacga gttaagcttc | 2220 |
| caagggatga ttcagacaaa tatagcttcc aagactcaaa ggcatgttgt cagaaggcca | 2280 |
| gtatttgttt cttcgaacga tgtggagcag aagagaagag gtccagagtg a | 2331 |

<210> 3
 <211> 78
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> PCR Primer

| | |
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| <400> 3 | |
| ataagcttgc caccatggct tstccststg stgttccaga tatgctgaat tcggcggccg | 60 |
| cgccaagttg accagtgc | 78 |

<210> 4
 <211> 26
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> PCR Primer

| | |
|-----------------------------|----|
| <400> 4 | |
| atategattc agtctgctc ctcggc | 26 |

<210> 5
 <211> 38
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Oligonucleotide

| | |
|---|----|
| <400> 5 | |
| ctagataact tcgtataatg tatgctatac gaagttat | 38 |

<210> 6
<211> 38
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide

<400> 6
ctagataact tcgtatagca tacattatac gaagttat 38

<210> 7
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR Primer

<400> 7
gcttatccat atgatgttcc agatt 25

<210> 8
<211> 34
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR Primer

<400> 8
atataggcgg cgcacctctg gacctcttct cttc 34

<210> 9
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR Primer

<400> 9
gagctctctg ggcttaacc 19

<210> 10
<211> 34
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR Primer

<400> 10
atatagcgcg cgcacctctg gacctcttct cttc

34

<210> 11
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> peptide

<400> 11

Cys Arg Arg Lys Tyr Cys Gln Arg Pro Cys Asp Ser Leu His
1 5 10

<210> 12
<211> 23
<212> PRT
<213> Artificial Sequence

<220>
<223> peptide

<400> 12

Cys Lys Leu Asn Leu Leu Gly Arg Cys His Tyr Ala Gln Ser Gln Arg
1 5 10 15

Asn Leu Cys Lys Tyr Ser His
20

<210> 13
<211> 23
<212> PRT
<213> Artificial Sequence

<220>
<223> peptide

<400> 13

Cys Lys Ser Tyr Lys Gly Glu Gly Arg Lys Gln Thr Cys Gly Gln Pro
1 5 10 15

Gln Pro Cys Glu Arg Leu His
20

<210> 14
<211> 18

<212> PRT

<213> Artificial Sequence

<220>

<223> peptide

<400> 14

Cys Glu His Phe Thr Arg Gly Asn Cys Ser Tyr Leu Asn Cys Leu Arg

1

5

10

15

Ser His